Wood anatomy and taxonomy of members of the genus *Ocimum* L. (Lamiaceae) and a variety in Nigeria

O.T. Oladipo, A.O. Oyaniran
Department of Botany, Obafemi Awolowo University, Ile-Ife, Nigeria

Wood anatomy of three species of *Ocimum* Linn. and a variety namely *O. basilicum*, *O. canum*, *O. gratissimum* and *O.basilicum* var. *purpurasens* found in Ile-Ife Nigeria was investigated. This was done with a view to discovering additional characters that may be diagnostic and important in the identification and classification of the members of the genus. Anatomical procedures were carried out on the matured stem of each species after the collection of the sample from the field. Wood samples were sectioned into Transverse, Tangential longitudinal and Radial longitudinal sections with the aid of Sledge microtome. Safranin O and Alcian blue were used for staining. Small quantity of Potassium dichromate and 10% Nitric acid were used for maceration. Permanent slides were prepared and microscopic observation was done under different objective lenses to view vessel elements, parenchyma cells, libriform fibre, and rays of various shapes. The length and diameter of vessels, fibre length and height of ray cells were taken using ocular micrometer at × 40 objective lens and Statistical analysis was carried out using one way analysis of variance (ANOVA) with Mean separation using Duncan Multiple Range Test (DMRT). Intra generic wood anatomical characters of note in the genus include- diffuse vessel elements, presence of uniseriate and biseriate rays, opposite inter vascular pitting and oblique vessel end walls. multiseriate rays are diagnostic of *O. gratissimum*. Overall results show high level relatedness between O.basilicum *var.purpurascens* and *O. gratissimum* as against *O. basilicum*.

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A survey of morphological and anatomical characters in the subtribe Phymaspermineae (Anthemideae, Asteraceae)

A.K. Ruiters[a], A.R. Magee[a,b], P.M. Tilney[a], B.-E. Van Wyk[a]
[a]*Department of Botany and Plant Biotechnology, University of Johannesburg, P.O. Box 524, Auckland Park 2006, Johannesburg, South Africa*
[b]*South African National Biodiversity Institute, Compton Herbarium, Private Bag X7, Claremont 7735, South Africa*

The tribe Anthemideae of Asteraceae has been recently revised to now include a new subtribe Phymasperminae. This modification accommodates new molecular data. The earliest diverging lineages of the tribe have their centres within southern Africa and it is therefore thought that the Anthemideae have originated in this region. Phymasperminae which is one of six of these lineages, comprises three genera: *Eumorphia* (6 spp.), *Gymnopentzia* (1 sp.) and *Phymaspermum* (ca. 19 spp.). Generic and species delimitations and relationships within the subtribe are unclear. This study attempts to divide the main genus *Phymaspermum* into more manageable informal groups as well as to determine the relationships between these species and the species of *Eumorphia* and *Gymnopentzia*. Five groups around *P. acerosum*, *P. athanasioides*, *P. parvifolium*, *P. erubescens* and *P. scoparia* were identified according to their habit and floral morphology. The results of a detailed morphological and anatomical study (using light and scanning electron microscopy) of subtribe Phymasperminae is presented. The shape of the involucre, the number and shape of the bracts, the presence and number of paleae as well as the number of florets were found to be taxonomically useful in distinguishing between species and species groups. Several fruit characters were also found to be taxonomically useful, such as the number of ribs, the presence of a pappus, myxogenic trichomes and resin canals.

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A phylogenetic classification of Asphodelaceae subfamily Alooideae

J.S. Boatwright[a], J.C. Manning[b], B.H. Daru[c], O. Maurin[c], M. Van der Bank[c]
[a]*Department of Biodiversity and Conservation Biology, University of the Western Cape, Private Bag X17, Belville 7535, Cape Town, South Africa*
[b]*Compton Herbarium, South African National Biodiversity Institute, Private Bag X7, Claremont 7735, Cape Town, South Africa*
[c]*Department of Botany and Plant Biotechnology, University of Johannesburg, P.O. Box 524, Auckland Park 2006, Johannesburg, South Africa*

The family Asphodelaceae arguably contains some of the best known horticultural and medicinal plant species in the world. Subfamily Alooideae currently comprises five genera mostly centred within southern Africa, with only *Aloe* extending to Madagascar, Arabia, the Canaries and the Comoros. The genera are largely diagnosed by overlapping suites of homoplasious morphological character states. Results from the analysis of plastid (*rbcLa*, *matK*, *trnH-psbA* and the *trnL* intron) and nuclear (ITS1) sequence datasets in a large sampling of species are presented. Only the two small genera *Astroloba* and *Gasteria* are recovered as well-supported monophyletic lineages. *Haworthia*, as also indicated by previous studies, is clearly polyphyletic as presently circumscribed, with the species distributed among three clades corresponding to the current subgenera. *Aloe* (with the inclusion of *Chortolirion*) segregates into five, well-supported monophyletic lineages corresponding respectively to sections *Dracoaloae*, *Kumara*, *Macrifoliae*, *Aristatae*, and the remainder of the genus. Sect *Aristatae* is strongly supported as a member of a clade comprising *Astroloba* + *Haworthia* subg. *Robustipedunculares*. The relationships among the remaining four *Aloe* lineages are, however, poorly resolved and, although indicative that *Aloe* may be polyphyletic, not conclusive at this stage. Significant generic recircumscriptions are indicated by the results and possible options are examined. Although morphological and molecular data are both consistent with expansion of the genus *Aloe* to include all members of Alooideae, thereby returning to Salm-Dyck's (1836–63) conception of the genus, we propose a more conservative and likely more generally acceptable option. *Astroloba* and *Gasteria* are retained as currently circumscribed; *Haworthia* is split into three genera corresponding with the current subgenera; and *Aloe* sect. *Aristatae* is now treated as a new genus. The four remaining lineages in *Aloe* are treated as subgenera. This treatment renders all seven genera arguably monophyletic in available molecular analyses, with minimal nomenclatural disruption.

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The split-tongue Ascleps and their cousins - an overview

S.P. Bester[a,b,c], A. Nicholas[c]
[a]*South African National Biodiversity Institute, Private Bag X101, Pretoria 0001 South Africa*
[b]*School of Environmental Sciences and Development, North-West University, Private Bag X6001, Potchefstroom 2520, South Africa*
[c]*School of Biology and Conservation Science, University of KwaZulu-Natal, Private Bag X54001, Durban 4000, South Africa*

The last full revision of *Schizoglossum sensu lato* was done by N.E. Brown in the Flora of tropical Africa (1902–1903) and Flora Capensis

(1909) respectively. A.A. Bullock did some work in the genus on the tropical African taxa in 1952–1963. In 1984 F. Kupicha partly revised the genus and split it into *Schizoglossum s.s.*, *Miraglossum* and *Aspidoglossum*. Despite this revision many taxa remained unresolved in *Schizoglossum s.l.* These 59 residual names left in *Schizoglossum* were merely informally assigned to prospective groups which are *Glossostelma* (7 taxa), *Pachycarpus* (19 taxa), *Stensotelma* (8 taxa), one group allied to *Aspidoglossum* but not congeneric to that genus (14 taxa) and the remaining 11 taxa with uncertain/unknown affinity. Except for the recent work by D. Goyder on the tropical taxa effectively this group of residual names have not received any taxonomic attention since Brown's work. More than half of these are restricted to southern Africa. In this presentation an overview of and outline for the proposed revision of the split-tongues (*Aspidoglossum, Miraglossum* and *Schizoglossum s.s.*) and their cousins (*Aspidonepsis, Cordylogyne, Periglossum* and *Stenostelma*) is given. Historically the flower and corona-structure are the most important diagnostic characters used in the generic and specific circumscriptions of these groups. However, global studies in the Asclepiadoideae have now show many previously used coronal-structures are not homologous and due to convergent evolution rather than ancestry. In this talk, these previously used diagnostic morphological characters are compared and illustrated. In the final formal revision of the group we aim to determine whether these characters and the DNA-data of their species are correlated. If this is the case then both sources of evidence will be used towards producing a concordant phylogeny and classification for this recently evolved complex of taxa.

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Phylogenetic and evolutionary studies of the family Thymelaeaceae in southern Africa

O. Maurin[a], J.S. Boatwright[b], J.C. Manning[c], M. Van der Bank[a]
[a]*African Centre for DNA Barcoding, University of Johannesburg, P.O. Box 524, Auckland Park 2006, Johannesburg, South Africa*
[b]*Department of Biodiversity and Conservation Biology, University of the Western Cape, Private Bag X17, Belville 7535, Cape Town, South Africa*
[c]*Compton Herbarium, South African National Biodiversity Institute, Private Bag X7, Claremont 7735, Cape Town, South Africa*

The family Thymelaeaceae comprises about 800 species distributed across 45 genera that occur in many parts of the tropics and Neotropics and display a wide range of diagnostic features. Several of the genera occur in Africa (*Craterosiphon*, *Dais*, *Dicranolepis*, *Englerodaphne*, *Gnidia, Lachnaea*, *Lasiosiphon, Octolepis, Peddiea, Struthiola, Synandrodaphne,* and *Synaptolepis*) and many are in need of revision and phylogenetic study due to unsatisfactory or uncertain generic circumscription. The main problems in the classification are within the subfamily Thymelaeoideae and revolve around the unplaced species of the dismembered genus *Arthrosolen,* the recently reinstated genus *Lasiosiphon* and the polyphyly of *Gnidia,* which impacts on the genera *Lachnaea, Passerina,* and *Struthiola.* In this study, we present the current state of knowledge, the taxonomic issues and phylogenetic relationships of the southern African Thymelaeaceae based on DNA sequences from both plastid (*matK, rbcL, trnH-psbA*) and nuclear (ITS) data sets as well as morphological data. The study aims to sample the remaining poorly studied genera or species and to propose a revised classification. The options available to achieve this will be discussed.

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Counterintuitive performance of core DNA barcodes within clades of southern African Combretaceae

J. Gere, K. Yessoufou, O. Maurin, L.T. Mankga, B.H. Daru, M. Van der Bank
African Centre for DNA Barcoding, Department of Botany & Plant Biotechnology, University of Johannesburg, South Africa

Recent studies indicate that the core DNA barcodes for land plants may have been overrated because its performance has arguably been tested using only few closely related species. In this study, we examined species discrimination within southern African Combretaceae using the core barcodes but also the combination core + supplementary barcodes. First, we tested the discriminatory power of single and gene combinations within the family as a whole. As expected, we found that the core barcode performed poorly compared to core + *trnH-psbA* or core + nrITS. Due to some limitations found for nrITS, we suggest that the core + *trnH-psbA* have greater barcode potential for the family. Second, based on the most recent and largest phylogeny available for the family, we identified major clades, and tested the efficacy of both core and core + *trnH-psbA* in discriminating species within five subsections (Angustimarginata, Ciliatipetala, Conniventia, Hypocrateropsis, Macrostigmatea) and the two subgenera (*Combretum* and *Cacoucia*) of the largest genus *Combretum*. In general, our results validate the lower performance of the core barcodes. Surprisingly however, we found that, in subsection Macrostigmatea, the performance of core barcodes surpasses by far not only its own performance (compared to the rest of the subsections tested), but more interestingly, the core barcodes outperform even the core + *trnH-psbA*. Our results indicate that the success of DNA barcode in discriminating closely related species may be contingent upon the evolutionary and possibly the biogeographic histories of the taxonomic group tested.

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Phylogeny of African Bruchids and their host plant *Acacia* species

A. Barker, N.P. Barker, M. Villet
Botany Department, Rhodes University, Grahamstown 6140, South Africa

Seed beetles, (Chrysomelidae: Bruchinae) are globally distributed and include approximately 60 genera and 1700 species. Many bruchine beetles are found on host plants from a narrow selection of species in the legume family (Leguminosae / Fabaceae). Bruchine larval stages develop exclusively inside the seeds of these plants. Studies of host-parasite co-evolution at the species level can therefore be explored within this group of beetles. Co-evolutionary studies of bruchines have been restricted to crop plant parasitism, and studies focussing on African bruchines are non-existent. We present results of a phylogeographic and co-evolutionary exploration of the South African bruchines that complete their life cycle on host plant genus Acacia. Mitochondrial DNA sequences from collected samples within the South African distribution range of the beetles were aligned with existing GenBank data, and paired phylogenies of beetles and host plants were generated. The comparison of host and parasite phylogeographic patterns, contrasted with previous studies of host-parasite interactions in other groups of bruchines assessed the co-evolutionary dynamics of this host-parasite relationship.

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